

09500746-020900

FIG. 1

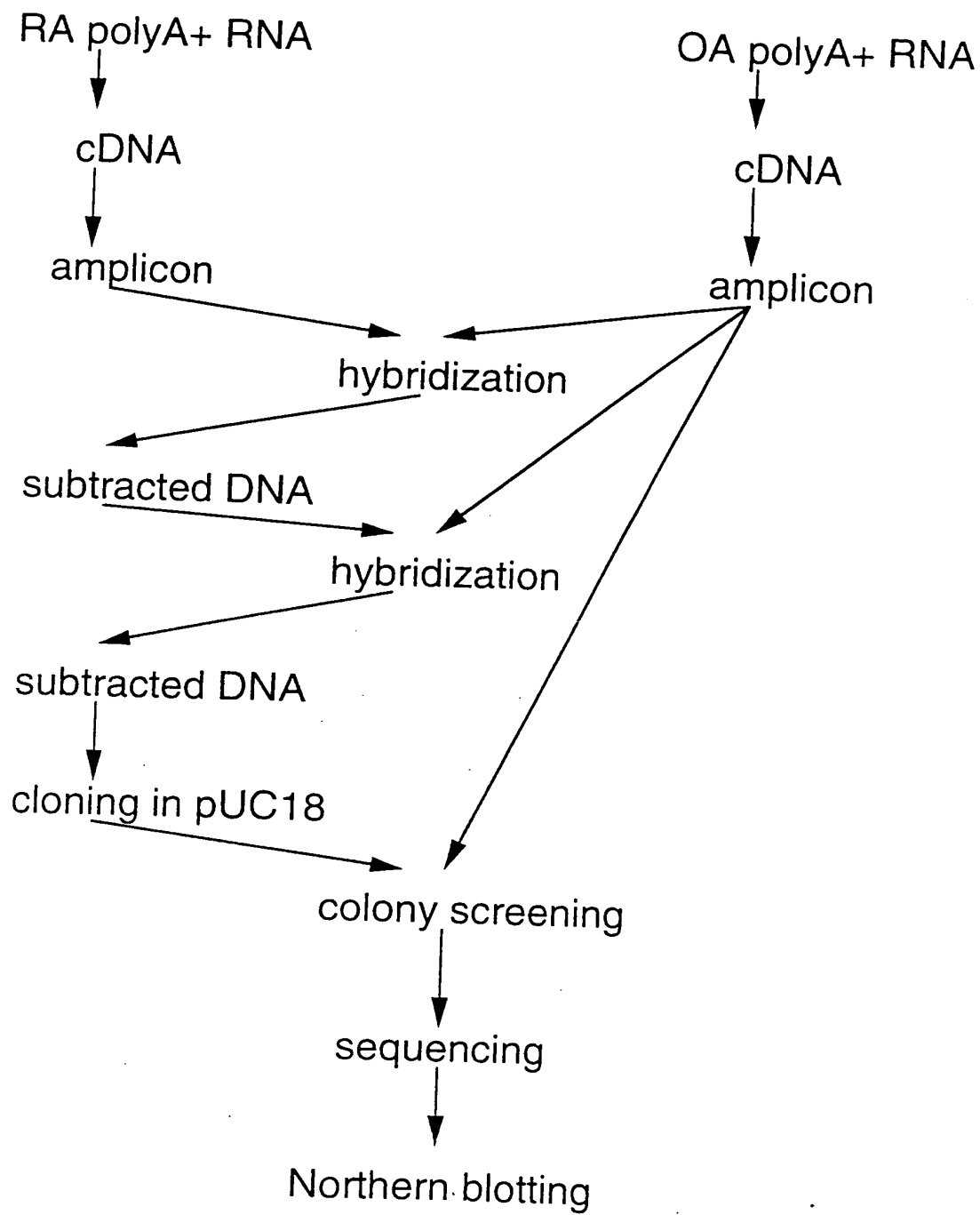


FIG. 2

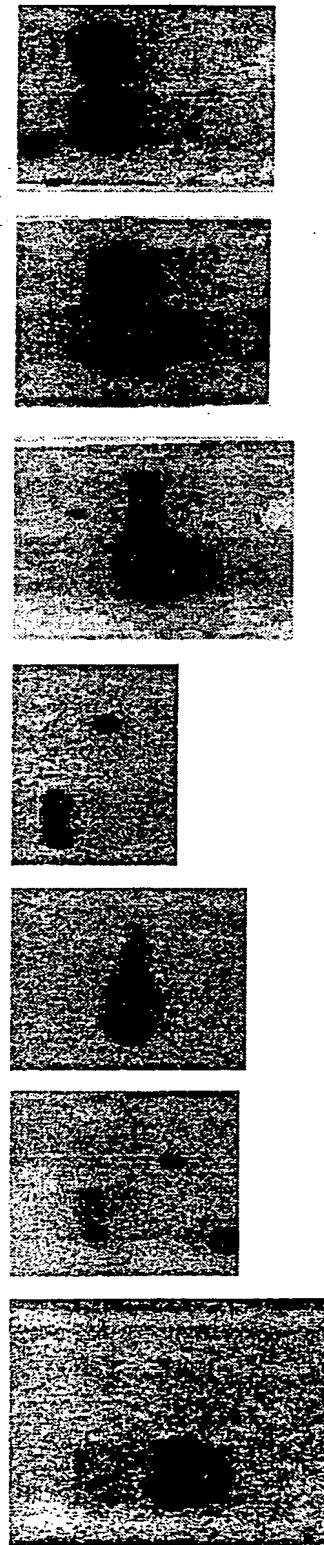
SAVCVYHLS	DIQ	TVFN	GPFA	HKEG	PNHQ	LISY	QGR	I	PYP	R	m	semaphor	in E								
SAVCVYHLS	DIQ	TVFN	GPFA	HKEG	PNHQ	LISY	QGR	I	PYP	R	h	semaphor	in VI								
SAVCVYHLS	DIQ	TVFN	GPFA	HKEG	PNHQ	LISY	QGR	I	PYP	R	h	semaphor	in IV								
SAVCVYHLS	DIQ	TVFN	GPFA	HKEG	PNHQ	LISY	QGR	I	PYP	R	h	semaphor	in V								
SAVCVYHLS	DIQ	TVFN	GPFA	HKEG	PNHQ	LISY	QGR	I	PYP	R	h	semaphor	in II								
PGTCPGG	AET	PNM	R	T	TKD	FPDD	V	VT	F	IRN	HPL	M	YN	S	I	SP	I	m	semaphor	in E	
PGTCPGG	ALT	PNM	R	T	TKD	FPDD	V	VT	F	IRN	HPL	M	YN	S	I	SP	I	h	semaphor	in VI	
PGTCPGG	FTT	PNM	R	T	TKD	FPDD	V	VT	F	IRN	HPL	M	YN	S	I	SP	I	h	semaphor	in IV	
PGMCP	SKT	FTT	PNM	R	T	TKD	FPDD	V	VT	F	IRN	HPL	M	YN	S	I	SP	I	h	semaphor	in V
PGTCP	SKT	FTT	PNM	R	T	TKD	FPDD	V	VT	F	IRN	HPL	M	YN	S	I	SP	I	h	semaphor	in II
HRRL	I	VR	I	G	T	D	Y	K	T	K	I	A	V	D					m	semaphor	in E
HRRL	I	VR	I	G	T	D	Y	K	T	K	I	A	V	D					h	semaphor	in VI
QRRL	I	VR	I	G	T	D	Y	K	T	K	I	A	V	D					h	semaphor	in IV
GRRL	I	VR	I	G	T	D	Y	K	T	K	I	A	V	D					h	semaphor	in V
NNRL	I	VR	I	G	T	D	Y	K	T	K	I	A	V	D					h	semaphor	in II

FIG. 3

S	Y	P	A	P	H	G	P	E	D	P	A	P	Q	F	A	H	M	F	E	N	E	I	S	H	R	T	G	S	W	N	F	A	P	N	P	D	K	Q	W	L	Q	R	T	CELK09C4	
S	H	A	A	P	H	G	P	E	D	S	A	P	Q	F	S	E	L	Y	P	N	A	S	Q	H	I	T	P	S	Y	N	Y	A	P	N	M	D	K	H	W	I	M	Q	Y	T	ts99
A	T	P	A	P	H	S	P	W	T	A	A	P	Q	Y	Q	K	A	F	Q	N	V	F	A	P	R	N	K	N	F	N	I	H	G	T	N	K	H	W	L	I	R	Q	A	K	GL6SHUMAN
G	K	M	N	D	V	H	I	S	F	T	D	L	L	H	R	R	R	L	Q	T	L	Q	S	V	D	E	G	I	E	R	L	F	N	L	L	R	E	L	N	Q	L	W	N	T	CELK09C4
G	P	M	L	P	I	H	M	E	F	T	N	I	L	Q	R	K	R	L	Q	T	L	M	S	V	D	D	S	V	E	R	L	Y	N	M	L	V	E	T	G	E	L	E	N	T	ts99
T	P	M	T	N	S	S	I	Q	F	L	D	N	A	F	R	K	R	W	Q	T	L	L	S	V	D	D	L	V	E	K	L	V	K	R	L	E	F	T	G	E	L	N	N	T	GL6SHUMAN
Y	A	I	Y	T	S	D	H	G	Y	H	L	G	Q	F	G	L	L	K	G	K	N	M	P	Y	E	F	D	I	R	V	P	F	F	M	R	G	P	G	I	P	R	CELK09C4			
Y	I	I	Y	T	A	D	H	G	Y	H	I	G	Q	F	G	L	V	K	G	K	S	M	P	Y	D	F	D	I	R	V	P	F	F	I	R	G	P	S	V	E	P	ts99			
Y	I	F	Y	T	S	D	N	G	Y	H	T	G	Q	F	S	L	P	I	D	K	R	Q	L	Y	E	F	D	I	K	V	P	L	L	V	R	G	P	G	I	K	P	GL6SHUMAN			

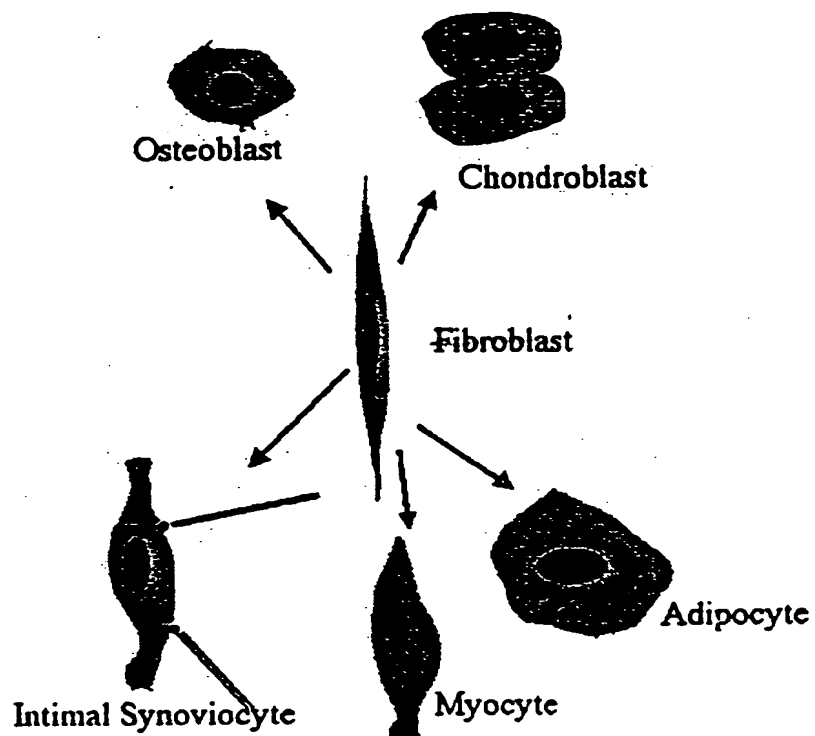
FIG. 4

RA OA RA OA RA OA RA OA RA OA RA OA RA OA



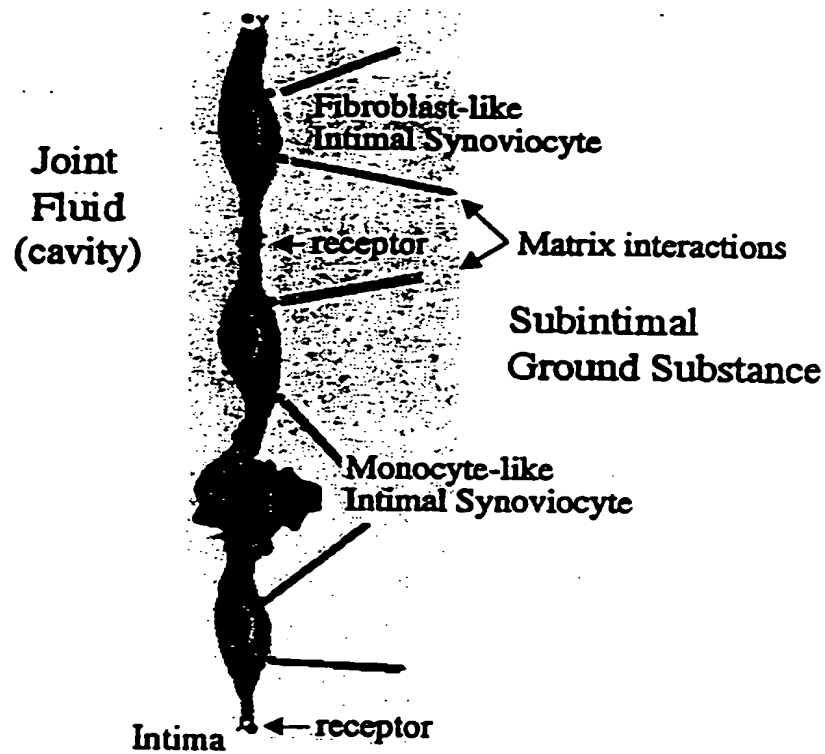
ML2122 ML2115 lumican IGFBP5 SDF1a semVI collagenaseIV

FIGURE 5



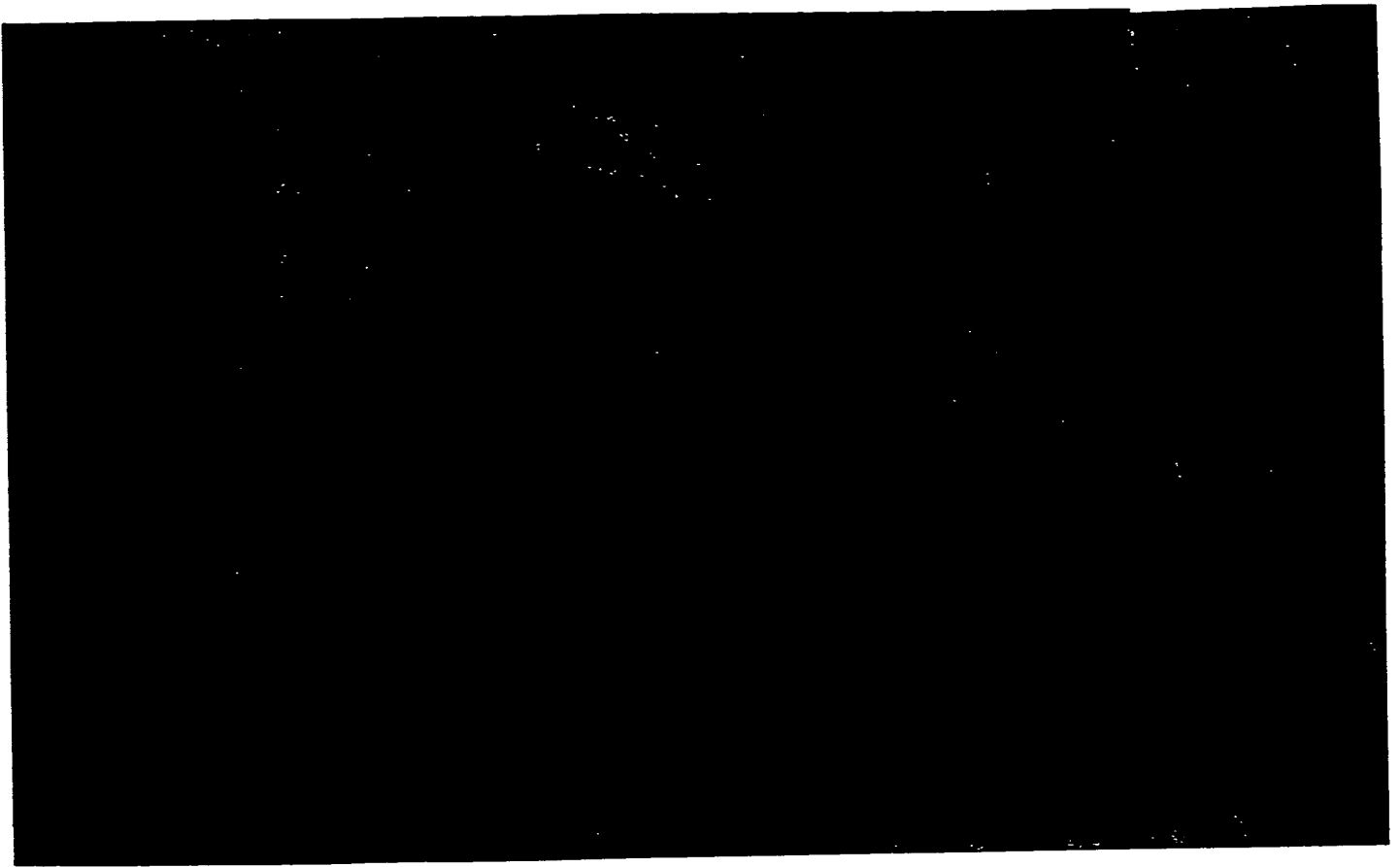
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FIGURE 6



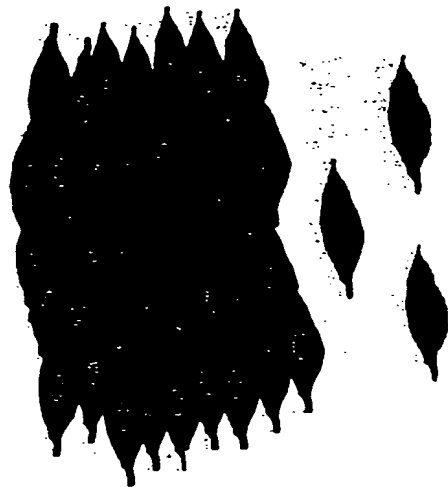
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FIGURE 7



□

FIGURE 8



Fibroblast-like intimal  
synoviocytes hyperplasia

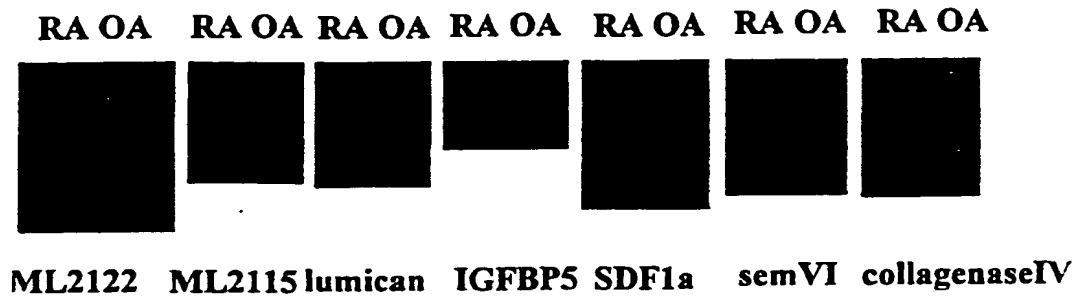


Subintimal fibroblast-like  
synoviocyte predominance

09500745 020900



FIGURE 9



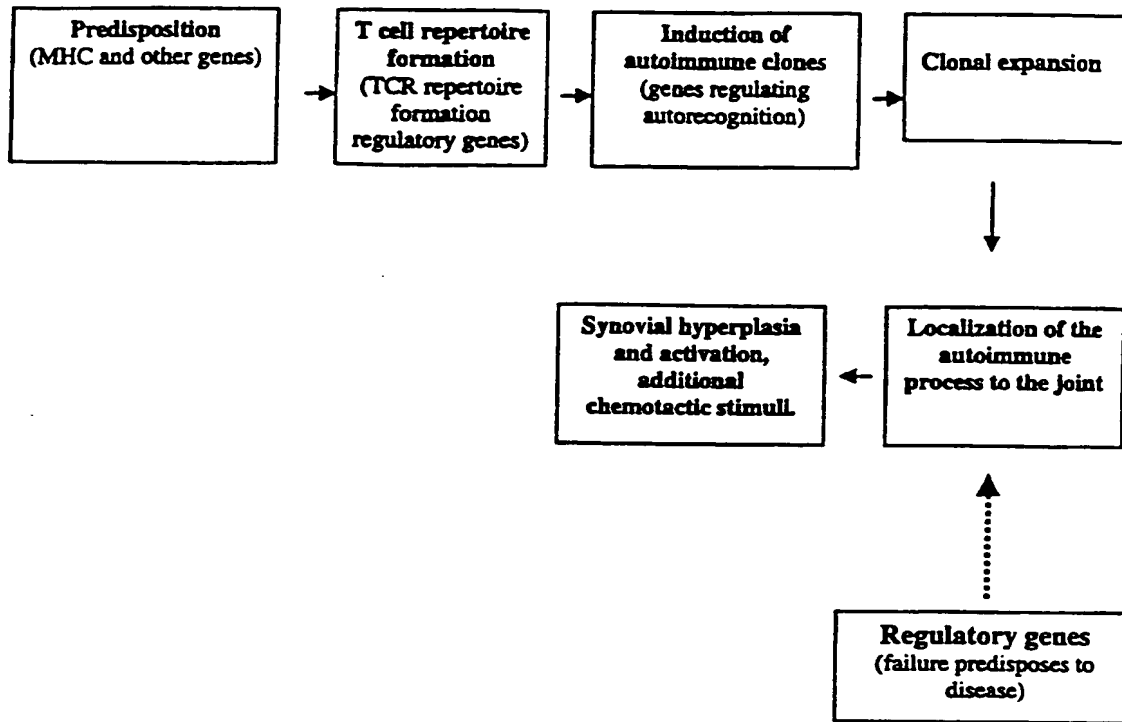
006020" 94200560

FIGURE 10

<b>ROLLING</b> selectins CD44	<b>TRIGGERING</b> chemokine-R integrins	<b>TIGHT BINDING</b> chemokine-R VCAM-1/ICAM-1 integrins	<b>TRANSMIGRATION</b> chemokine-R integrins
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006020 " 94/00560

FIGURE 11



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FIGURE 12

			10	20	30	40	50	60
New 95-04-12- 25.Seq(1>484)	<-	GNNGAGTGTGGGACGGGGGNGNAGNAATTAAGGTAGNG-ATGGAGNANGGGGTGCNTNNG						
New 95-04-12- 27.Seq(1>437)	->	CCCCGGGTACCGAGCTCGAATTCCGTTG						
		GXXGAGTGTGGGACGGGGGXXGAXAATTAAGSYMGGGTAYSAGAGCWCGRRTSCGTTG						
			70	80	90	100	110	120
New 95-04-12- 25.Seq(1>484)	<-	GNNNAGANANTGNNTGGAGAANGACAANGGGGGGNGTCGNNGGAGGNGNTGTGA-GTGGG						
New 95-04-12- 27.Seq(1>437)	->	NTGTCGCCCGTTGN-TGTCG-----CAGATGCCCATGCCGATTCTTCGAAAGCCATGTTGC						
New 95-04-12- 01.Seq(1>382)	->	CAGATGCCCATGCCGATTCTTCGAAAGCCATGTTGC						
New 95-03-30- 34.Seq(1>439)	->	CAGATGNCCATGCCGATTCTTCGAAAGCCATGTTGC						
New 95-04-12- 21.Seq(1>466)	<-	CCATGTTCC						
		GTGTMGMCRTTGXX-TGKMGaaxgaCAGATGSCCATGCCGATTCTTCGAAAGCCATGTTGC						
			130	140	150	160	170	180
New 95-04-12- 25.Seq(1>484)	<-	AAGAAGGCNACGTCAANAAGGACGAATATTTGCAANGNNGNNCAGGGCTGTNCNCGGGCA						
New 95-04-12- 27.Seq(1>437)	->	CAGA-GCCAACGTCAAGCATCTCAAA-ATTCTCAACACTCC-AAA--CTGTGCCCTT-CA						
New 95-04-12- 01.Seq(1>382)	->	CAGA-GCCAACGTCAAGCATCTCAAA-ATTCTCAACACTCC-AAA--CTGTGCCCTT-CA						
New 95-03-30- 34.Seq(1>439)	->	CAGA-GCCAACGTCAAGCATCTCAAA-ATTCTCAACACTCC-AAA--CTGTGCCCTT-CA						
New 95-04-12- 21.Seq(1>466)	<-	AAGA-NCCA-CGTCAA-CATCCCAA-AT-CTCAACACNCC-CAA--CTNTTCCCTT-CA						
		MAGA-GCCAACGTCAAGCATCTCAAA-ATTCTCAACACTCC-MAA--CTGTGCCCTT-CA						
			190	200	210	220	230	240
New 95-04-12- 25.Seq(1>484)	<-	GTTTGTAAAAAANAAGAACNGCGACAGACAAGTGTNNG-TTGACCCGAAGC-NA						
New 95-04-12- 27.Seq(1>437)	->	GATTGTAGCCCGGCTGAAGAACAACAAC-A--GACAAGTGTGCA-TTGACCCGAAGCTAA						
New 95-04-12- 01.Seq(1>382)	->	GATTGTAGCCCGGCTGAAGAACAACAAC-A--GACAAGTGTGCA-TTGACCCGAAGCTAA						
New 95-03-30- 34.Seq(1>439)	->	GATTGTAGCCCGGCTGAAGAACAACAAC-A--GACAAGTGTGCA-TTGACCCGAAGCTAA						
New 95-04-12- 21.Seq(1>466)	<-	GATTGTAGCCCGGCTGAAGAACAACAAC-A-AGACAAGTGTGCA-TTGACCCGAAGCTAA						
		GATTGTAGCCCGGCTGAAGAACAACAAC-A-aGACAAGTGTGCA-TTGACCCGAAGCTAA						
			250	260	270	280	290	300
New 95-04-12- 25.Seq(1>484)	<-	NAGTGGATNCAGGAGTACC-TGGAGNNA-CTATGAACAANTAAGCGCAACAGCC-AAAG						
New 95-04-12- 27.Seq(1>437)	->	A-GTGGATTACAGGAGTACC-TGGAG-AAAGCTTTAAACAAGTAAGCACAACAGCC-AAAA						
New 95-04-12- 01.Seq(1>382)	->	AAGTGGATTACAGGAGTACC-TGGAGAAAGCTTTAAACAAGTAAGCACAACAG-CCAAAA						
New 95-03-30- 34.Seq(1>439)	->	AAGTGGATTACAGGAGTACC-TGGAGTAAAGCTTTAAACAAGTAAGCACAACAG-NCAAAA						
New 95-04-12- 21.Seq(1>466)	<-	AAGTGGATTACAGGAGTACC-TGGAGAAAGCTTTAAACAAGTAAGCACAACAGCCCAAAA						
		AAGTGGATTACAGGAGTACC-TGGAGkAAAGCTTTAAACAAGTAAGCACAACAGCcCAAAA						
			310	320	330	340	350	360
New 95-04-12- 25.Seq(1>484)	<-	AGGACTTTCGCTAGACCCACTCGAGGAAAACTAAAACCTTGTGAGAGATGAAAGGNCAA						
New 95-04-12- 27.Seq(1>437)	->	AGGACTTTCGCTAGACCCANTCGANGAAAACTAAAACCTTGTGAGAGATGAAAGGGCAA						
New 95-04-12- 01.Seq(1>382)	->	AGGACTTTCGCTAGACCCACTCGAGGAAAACTAAAACCTTGTGAGAGATGAAAGGGCAA						
New 95-03-30- 34.Seq(1>439)	->	AGGACTTTCGCTAGACCCACTCGAGGAAAACTAAAACCTTGTGAGAGATGAAAGGGCAN						
New 95-04-12- 21.Seq(1>466)	<-	AGGACTTTCGCTAGACCCACTCGAGGAAAACTAAAACCTTGTGAGAGATGAAAGGNCAA						
New 95-04-12- 19.Seq(1>463)	<-	AN-TGAAGGGCCAA						
		AGGACTTTCGCTAGACCCACTCGAGGAAAACTAAAACCTTGTGAGAGATGAAAGGSCAA						
			370	380	390	400	410	420
New 95-04-12- 25.Seq(1>484)	<-	AGACGTGGGGG-AGGGGGCCNTAAC-CA-TGAGGACCAGGTGTGTGTGTGGGG-TGGG-C						
New 95-04-12- 27.Seq(1>437)	->	AGACGTGGGGGGAGGGGGGCTTAAC-CA-TGAGGACCAGGTGTGTGTGT-NGGGTGGGGC						
New 95-04-12- 01.Seq(1>382)	->	NGACGTNGNGG-AGGGGGGCTTAACC-AT-GAGGACCAGGTGTGTGTNTGGGGGTGGG-T						
New 95-03-30- 34.Seq(1>439)	->	TGTNTTGTGG-AGGGGGCCTTAACC-AT-GAGGACCAGGTGTGTGTGTGGGG-TGGG-C						
New 95-04-12- 21.Seq(1>466)	<-	AGACGTGGGGG-AGGGGGCCTTAACC-CA-TGAGGACCAGGTGTGTGTGTGGGG-TGGG-C						
New 95-04-12- 19.Seq(1>463)	<-	AGACGTGGGGG-AGGGGGCCTTAACCCATTGAGGACCAGNTGTGTGTGTGGGGGTGGC-C						
		WGACGTGKGGG-AGGGGGSCCTTAACccAttGAGGACCAGGTGTGTGTGTGGGGgTGGG-C						
			430	440	450	460	470	480
New 95-04-12- 25.Seq(1>484)	<-	ACATTG-ATCT-GGG-ATCGGGCCTGAGGTTTGCCAGCATTTAGACCCTGCATTTATAGC						
New 95-04-12- 27.Seq(1>437)	->	ACATTGGATCTTN-G-ATCGGGCCTGAGGTTTGGCAGCATTTAGACCCTGGATTTAT-GN						
New 95-04-12- 01.Seq(1>382)	->	ACATTGNATCTTGGG-ATCGGGCCTGAGGTTTNGGCAGAATTTNGNCCCTGNATTTATNGN						
New 95-03-30- 34.Seq(1>439)	->	ACATNGNATCT-GGGTATCGGGCCTGAGGTTTGNACAGCATTTAGNCCCTGNATTTATNGC						
		ACATTGxATCTtGGG-ATCGGGCCTGAGGTTTGSACAGCATTTAGACCCTGSATTTATRG						

430 440 450 460 470 480

New 95-04-12- 21.Seq(1>466) <- ACATTG-ATCT-GGG-ATCGGGCTGAGGTTTGCCAGCATTTAGACCTGCATTTATAGC  
New 95-04-12- 19.Seq(1>463) <- ACATTG-ATCT-GGG-ATCGGGCTGAGGTTTGCCAGCATTTAGACCTGCATTTATAGC  
ACATTGxATCTtGGG-ATCGGGCTGAGGTTTGSCAGCATTTAGACCTGSATTTATRGC  
490 500 510 520 530 540

New 95-04-12- 25.Seq(1>484) <- ATACGGTATGATATTGCAG  
New 95-04-12- 27.Seq(1>437) -> ATACGNNITGATNINN  
New 95-04-12- 01.Seq(1>382) -> ATCC  
New 95-03-30- 34.Seq(1>439) -> ATACGGCATGATATTGCAGNTTAT-TTCATCCATGCCNCGTACCTGTGNACGTTGGGAC  
New 95-04-12- 21.Seq(1>466) <- ATACGGTATGATATTGCAGCTTATATTTCATCCATGCC- TGTACCTGTGCACGTTGGAAC  
New 95-04-12- 19.Seq(1>463) <- ATACGGTATGATATTGCAGCTTATATTTCATCCATGCC- TGTACCTGTGCACGTTGGAAC  
ATACGGYATGATATTGCAGCTTATATTTCATCCATGCCxYGTACCTGTGCACGTTGGRAC  
550 560 570 580 590 600

New 95-03-30- 34.Seq(1>439) -> TAG  
New 95-04-12- 21.Seq(1>466) <- TTTTATTACTGGGGTTTTTCTAAGAAAGAAATTGTATTATCAACAGCATTTTCA-GACA  
New 95-04-12- 19.Seq(1>463) <- TTTTATTACTGGGGTTTTTCTAAGAAAGAAATTGTATTATCAACAGCATTTTCAAG-CAG  
TWKTATTACTGGGGTTTTTCTAAGAAAGAAATTGTATTATCAACAGCATTTTCAaGaCAG  
610 620 630 640 650 660

New 95-04-12- 19.Seq(1>463) <- TTAGTTCCTTCATGATCATCACAATCATCATCATTCTCATTCTCATTTTTTAAATC-AAC  
New 95-04-12- 17.Seq(1>461) <- GGTTCATCNCAATCATCATCATTCTCATTCTCATTTTTTAAATCCAAC  
TTAGTTCCTTCATGRTCATCACAATCATCATCATTCTCATTCTCATTTTTTAAATCcAAC  
670 680 690 700 710 720

New 95-04-12- 19.Seq(1>463) <- GAGTACTTCAAGATCTGAATTTGGCTTGTTTGGAGCATCTCCTCTGCTCCCCCTGGGGAGT  
New 95-04-12- 17.Seq(1>461) <- GAGTACNTCAAGATCTG-ATTTGGCTTGTTTGGAGCATCTCCTCTGCTCCCCCTGGGGAGT  
GAGTACTTCAAGATCTGaATTTGGCTTGTTTGGAGCATCTCCTCTGCTCCCCCTGGGGAGT  
730 740 750 760 770 780

New 95-04-12- 19.Seq(1>463) <- CTGGGCACAGTCAGGTGGTGGCTTAACAGGGAGCTGGAAAAAGTGCCTTTCTTCAGACA  
New 95-04-12- 17.Seq(1>461) <- CTGGGCACAGTCAGGTGGTGGCTTAACAGGGAGCTGGAAAAAGTGCCTTTCTTCAGACA  
New 95-03-30- 09.Seq(1>445) -> GGGAGCTGGAAAAAGTGCCTTTCTTCAGACA  
CTGGGCACAGTCAGGTGGTGGCTTAACAGGGAGCTGGAAAAAGTGCCTTTCTTCAGACA  
790 800 810 820 830 840

New 95-04-12- 19.Seq(1>463) <- CTGAGGCTCCCCGAGCAGCGCCCCCTCCCAAGAGGAAGG  
New 95-04-12- 17.Seq(1>461) <- CTGAGNCTCCCCGAGCAGCGCCCCCTCCCAAGAGGAAGGCCCTCTGTGGCACTCAGATACCG  
New 95-03-30- 09.Seq(1>445) -> CTGAGGCTCCCCGAGCAGCGCCCCCTCCCAAGAGGAAGGCCCTCTGTGGCACTCAGATACCG  
CTGAGGCTCCCCGAGCAGCGCCCCCTCCCAAGAGGAAGGCCCTCTGTGGCACTCAGATACCG  
850 860 870 880 890 900

New 95-04-12- 17.Seq(1>461) <- ACTGGGGCTGGGCGCCGCCACTGCCTTCACCTCCTCTTTCAACCTCAGTGATTGGCTCTG  
New 95-03-30- 09.Seq(1>445) -> ACTGGGGNTGGGCGCCGCCACTGNCTTCACCTCCTCTTTCAACCTCAGTGATTGGCTCTG  
ACTGGGGCTGGGCGCCGCCACTGCCTTCACCTCCTCTTTCAACCTCAGTGATTGGCTCTG  
910 920 930 940 950 960

New 95-04-12- 17.Seq(1>461) <- TGGGCTCCATGTAGAAGCCACTATTACTGGGACTGTGCTCAGAGACCCCTCTCCCAGCTA  
New 95-03-30- 09.Seq(1>445) -> TGGGCTCCATGTAGAAGCCACTATTACTGGGACTGTGCTCAGAGACCCCTCTCCCAGCTA  
New 95-04-12- 03.Seq(1>447) -> CCCAGCTA  
TGGGCTCCATGTAGAAGCCACTATTACTGGGACTGTGCTCAGAGACCCCTCTCCCAGCTA  
970 980 990 1000 1010 1020

New 95-04-12- 17.Seq(1>461) <- TTCCTACTCTCTCCCCGACTCCGAGAGCATGCTTAATCTTGCTTCTGCTTCTCATTTCTG  
New 95-03-30- 09.Seq(1>445) -> TTCCTACTCTCTCCCCGACTCCGAGAGCATGCTTAATCTTGCTTCTGCTTCTCATTTCTG  
New 95-04-12- 03.Seq(1>447) -> TTCCTACTCTCTCCCCGACTCCGAGAGCATGCTTAATCTTGCTTCTGCTTCTCATTTCTG  
TTCCTACTCTCTCCCCGACTCCGAGAGCATGCTTAATCTTGCTTCTGCTTCTCATTTCTG

			1030	1040	1050	1060	1070	1080
New 95-04-12- 17. Seq(1>461)	<-	TAGCCTGATCAGCGCCGACCAGCCGGGAAGAGGGTGATTGCTGGGGCTCGTGCC						
New 95-03-30- 09. Seq(1>445)	->	TAGNCTGATCAGNGCCGACCAGCCGGGAAGAGGGTGATTGCTGGGGCTCGTGCCCTGCA						
New 95-04-12- 03. Seq(1>447)	->	TAGCCTGATCAGCGCCGACCAGCCGGGAAGAGGGTGATTGCTGGGGCTCGTGCCCTGCA						
New 95-04-12- 11. Seq(1>463)	<-						AG-TCGTGCCCTGCA	
New 95-04-12- 07. Seq(1>453)	->						TGCCCTGCA	
		TAGCCTGATCAGCGCCGACCAGCCGGGAAGAGGGTGATTGCTGGGGCTCGTGCCCTGCA						
			1090	1100	1110	1120	1130	1140
New 95-03-30- 09. Seq(1>445)	->	TCCCTCTCC-TCCCAGGGGCTGNCCCAC-AGNTC-GGGCCCT-CTGTGAGATCCG--CTI						
New 95-04-12- 03. Seq(1>447)	->	TCCCTCTCC-TCCCAGGGGCTGCCCCAC-AGCTC-GGGCCCT-CTGTGAGATCCGT-CTI						
New 95-04-12- 11. Seq(1>463)	<-	TCCCTCTCCCTCCCAGGNCCTTCCCCACAAGCTCGGGGCCCT-CTGTGAGACCCGT-CTI						
New 95-04-12- 07. Seq(1>453)	->	TCCCTCTCC-TCCCAGGGGCTGCCCCAC-AGCTC-GGGCCCT-CTGTGAGATCCGT-CTI						
New 95-04-12- 05. Seq(1>475)	->						CGACGNCAGTGCCAAGCTTGCAI	
		TCCCTCTCC-TCCCAGGGGCTGCCCCAC-AGCTC-GGGCCCT-CTGTGAGAHCCGT-CTI						
			1150	1160	1170	1180	1190	1200
New 95-03-30- 09. Seq(1>445)	->	TNGG-CTCCTCCAGAATGG-GNTGGCCC-CTCCTGGGGATGTGTAATGGTCCCCC-TGCT						
New 95-04-12- 03. Seq(1>447)	->	T-GGCCCTCCTCCAGAATGGAGCTGGCCCTCTCCTGGGGATGTGTAATGGTCCCCC-TGCT						
New 95-04-12- 11. Seq(1>463)	<-	T-GCCCTCCTCCAGAATGGAGCTGGCCCTCTCCTGGGGATGTGTAATGGTCCCCCTGCT						
New 95-04-12- 07. Seq(1>453)	->	T-GGCCCTCCTCCAGAATGGAGCTGGCCCTCTCCTGGGGATGTGTAATGGTCCCCC-TGCT						
New 95-04-12- 05. Seq(1>475)	->	---GCCTCCTCCAGAATGGAGCTGGCCCTCTCCTGGGGATGTGTAATGGTCCCCC-TGCT						
		T-GGCCCTCCTCCAGAATGGAGCTGGCCCTCTCCTGGGGATGTGTAATGGTCCCCC-TGCT						
			1210	1220	1230	1240	1250	1260
New 95-03-30- 09. Seq(1>445)	->	TAG						
New 95-04-12- 03. Seq(1>447)	->	TACCCGC-AAAAGACAAGTCTTTACAGAATCAAATGCAATTTTAAATCTGAGAGCTCGCT						
New 95-04-12- 11. Seq(1>463)	<-	TACCCCAAAAAGACAAGTCTTTACAGAATCAAATGCAATTTTAAATCTGAGAGCTCGCT						
New 95-04-12- 07. Seq(1>453)	->	TACCCGC-AAAAGACAAGTCTTTACAGAATCAAATGCAATTTTAAATCTGAGAGCTCGCT						
New 95-04-12- 05. Seq(1>475)	->	TACCCGC-AAAAGACAAGTCTTTACAGAATCAAATGCAATTTTAAATCTGAGAGCTCGCT						
		TACCCGC-AAAAGACAAGTCTTTACAGAATCAAATGCAATTTTAAATCTGAGAGCTCGCT						
			1270	1280	1290	1300	1310	1320
New 95-04-12- 03. Seq(1>447)	->	TTGAGTGACTGGGTTTTGGTGATTGNCCTCTGAAGCCTATGTATGCCATGGAGGGACTAAC						
New 95-04-12- 11. Seq(1>463)	<-	TTGAGTGACTGGGTTTTG-TGATTGCCTCTGAAGCCTATGTATGCCATGGAGGGACTAAC						
New 95-04-12- 07. Seq(1>453)	->	TTGAGTGACTGGGTTTTG-TGATTGCCTCTGAAGCCTATGTATGCCATGGAGGGACTAAC						
New 95-04-12- 05. Seq(1>475)	->	TTGAGTGACTGGGTTTTG-TGATTGCCTCTGAAGCCTATGTATGCCATGGAGGGACTAAC						
		TTGAGTGACTGGGTTTTG-TGATTGCCTCTGAAGCCTATGTATGCCATGGAGGGACTAAC						
			1330	1340	1350	1360	1370	1380
New 95-04-12- 03. Seq(1>447)	->	AAACTCTGAGGTTTCCGAAATCAGAAGCGAAAAA-TCAGTGAATAAACCATCATCTTGCC						
New 95-04-12- 11. Seq(1>463)	<-	AAACTCTGAGGTTTCCGAAATCAGAAGCGAAAAATCAGTGAATAAACCATCATCTTGCC						
New 95-04-12- 07. Seq(1>453)	->	AAACTCTGAGGTTTCCGAAATCAGAAGCGAAAAATCAGTGAATAAACCATCATCTTGNC						
New 95-04-12- 05. Seq(1>475)	->	AAACTCTGAGGTTTCCGAAATCAGAAGCGAAAAATCAGTGAATAAACCATCATCTTGCC						
		AAACTCTGAGGTTTCCGAAATCAGAAGCGAAAAATCAGTGAATAAACCATCATCTTGSC						
			1390	1400	1410	1420	1430	1440
New 95-04-12- 03. Seq(1>447)	->	ACTA-CCCCTCCTGAAGC-ACAGNAGGGTT						
New 95-04-12- 11. Seq(1>463)	<-	ACTACCCCTCCTGAAGCCACAGCAGGGTTTCAGGTTCCAATC-AGAAGTGTGGC-AAG						
New 95-04-12- 07. Seq(1>453)	->	ACTACCCCTCCTGAAGCCACAGCAGGGTTTCAGGTTCCAATC-AGAAGTGTGG-CAAG						
New 95-04-12- 05. Seq(1>475)	->	ACTACCCCTCCTGAAGCCACAGCAGGGTTTCAGGTTCCAATC-AGAAGTGTGG-CAAG						
New 95-03-30- 03. Seq(1>376)	<-						CNA-NNAGAACTGTTGCCCG-G	
New 95-03-30- 30. Seq(1>377)	<-						GATCAAGGGCTGTTGGCCGAG	
New 95-04-12- 09. Seq(1>381)	->						CTGTTGGCA-AG	
		ACTACCCCTCCTGAAGCCACAGCAGGGTTTCAGGTTCCRATCaAGAAGTGTGGcCRAG						
			1450	1460	1470	1480	1490	1500
New 95-04-12- 11. Seq(1>463)	<-	GT-GACATTTCCATGCATAAATGCGATCCACAGAAGGTCCTGGT-GGTATTT-GTAACCTI						
New 95-04-12- 07. Seq(1>453)	->	GT-GACATTTCCATGCATAAATGCGATCCACAGAAGGTCCTGGTGGGTATTTGGTAACCTI						
New 95-04-12- 05. Seq(1>475)	->	GT-GACATTTCCATGCATAAATGCGATCCACAGAAGGTCCTGGTGGGTATTTGGTAACCTI						
		GT-GACATTTCCATGCATAAATGCGAWCCACAGRRGGKCCTGGKgGGTATTTgGTAACYI						

1450 1460 1470 1480 1490 1500

New 95-03-30- 03.Seq(1>376) <- GT-GACATTTCCATNCATAAATGCGAACCACAGNNGGNCC-NGGNGGNA-TT-TNTACCT  
New 95-03-30- 30.Seq(1>377) <- GTGGNAATTTCCATNCANAAATGCGAACCCAGGGGGGCGGGGGGNA-TT-GTAACCT  
New 95-04-12- 09.Seq(1>381) -> GT-GACATTTCCATGCATAAATGCGATCCACAGAAGGTCTGGT-GGTATTT-GTAACTT  
GT-GACATTTCCATGCATAAATGCGAWCCACAGRRGGKCCCTGGKgGGTATTTgGTAACYT

1510 1520 1530 1540 1550 1560

New 95-04-12- 11.Seq(1>463) <- TTTGCAAGGCATTTTTTTTATATATAT-TTTTGTGGGCA  
New 95-04-12- 07.Seq(1>453) -> TTNGGAAGGNATTTNNNNATATATAT-TTTNGGGAN  
New 95-04-12- 05.Seq(1>475) -> TTGGNAAGGC-A-TTTNNNNATATATATTTNGGGGCACATTTTTTTTTTACGTTTCTTTT  
New 95-03-30- 03.Seq(1>376) <- TTTNCCAGGCAN-TTTTTTAAAAAAAANTTTGT-NCANATTTTTTTTACGNITCNTNA  
New 95-03-30- 30.Seq(1>377) <- TTTTCCAGGNAATTTTTTAAAAAAA-NTTTGT-GCACANTTTTTTTTNCGNITCNTNA  
New 95-04-12- 09.Seq(1>381) -> TTTGNAAGGCATTTTTTTATATATAT-TTTTGNG-CACATTTTTTTTTTACGTTTCTTTA  
TTKSMAGGCATTTTTTAWAWAWAWaTTTTGKgrSAMATTTTTTTTTTACGTTTCTTTA

1570 1580 1590 1600 1610 1620

New 95-04-12- 05.Seq(1>475) -> AGAAACAAATGT-TTTCAAAATNT-TTTAT-GGTCGACAATCAAT  
New 95-03-30- 03.Seq(1>376) <- GNAANCCAATGTATTTCCCAANATATTTANANGCGGACAANTC--ANATANTTGGAGTGG  
New 95-03-30- 30.Seq(1>377) <- GGANGCCNATNNATNCCCCANATGTTTATAGGCGNANAAAAA--AAAAATTTGGGGNGG  
New 95-04-12- 09.Seq(1>381) -> GAAAACAAATGTATTTCAAAATATATTTATAGTCGAACAAATTCAT--ATATTTGAAGTGG  
GRAARCMATGTATTTTCMAATATRTTTATAGGCGRACAAWHMatAaAWATTTGRRGTGG

1630 1640 1650 1660 1670 1680

New 95-03-30- 03.Seq(1>376) <- ANCCAAATGGATNTCAGTAGTTTAAACNTCTCTANTATCCCCAACNGCTGGCCANTTTNTT  
New 95-03-30- 30.Seq(1>377) <- NGCCAANTGGATTTTCAGGAGNTNAAACCTCNCNANTATCCCCNCCNCTGGCCATTTTTTT  
New 95-04-12- 09.Seq(1>381) -> AGCCATATGAATGTCAGTAGTTTATACTTCTCTATTATCTCAAACACTGGCAATTTGTA  
AGCCAWATGRATKTCAGKAGTTTAWACYTCTCTAXTATCYCMAACYRCTGGCMATTTKTW

1690 1700 1710 1720 1730 1740

New 95-03-30- 03.Seq(1>376) <- NAGNAANAAANATGAAAAANGAATNTGGTTTTCAGCNTTTCCATNTTAACNCAGTNGATT  
New 95-03-30- 30.Seq(1>377) <- AAGGNAAAAAAATGAAAAANNGAATNTGGTTTTCAGCCTTTCCATNTTAACNCAGTNNAAI  
New 95-04-12- 09.Seq(1>381) -> AAGAAATATATATGATATATAAATGTGATTGCAGCTTTTCAATGTTAGCCACAGTGTATI  
AAGRAAWAWAWATGAWAWAXRRATXTGRTTKCAGCYTTTCMATXTTARCCXCAGTXKAWI

1750 1760 1770 1780 1790 1800

New 95-03-30- 03.Seq(1>376) <- TTTTCACTTTNTNCCAAATNTTACCCNATNTNACANTAAATNCCCTANCNAANAATTCN  
New 95-03-30- 30.Seq(1>377) <- TTTTCNCTTTNNCCNNAATTTNNCCCCATNTNGCNTTAAATTTCCCNANCCAAANAATNCN  
New 95-04-12- 09.Seq(1>381) -> TTTTCACTTGTACTAAAATTTGTATCAAATGTGACATTATATGCACTAGCAATAAAATGCT  
TTTTCACTTXXTCYAAAATTTXTAYCMMATXTXRCATTAWATKCMCTAXCMAWAAAAATKCX

1810

New 95-03-30- 03.Seq(1>376) <- GATT  
New 95-03-30- 30.Seq(1>377) <- NA  
New 95-04-12- 09.Seq(1>381) -> AATTGTTTCATGGGTAA  
RATTGTTTCATGGGTAA